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0131 #13

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RAW SEQUENCE LISTING DATE: 08/07/2002
PATENT APPLICATION: US/09/964,275B TIME: 09:50:02

Input Set : A:\0136542 SEQLST.ST25.txt
Output Set: N:\CRF3\08072002\I964275B.raw

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 3 <110> APPLICANT: Dai, Ken-Shwo
 4       Yang, Chin-Chang
 6 <120> TITLE OF INVENTION: HUMAN NOC2-RELATED GENE VARIANTS ASSOCIATED WITH LUNG CANCER
 8 <130> FILE REFERENCE: U 013654-2
10 <140> CURRENT APPLICATION NUMBER: 09/964,275B
11 <141> CURRENT FILING DATE: 2001-09-26
13 <160> NUMBER OF SEQ ID NOS: 10
15 <170> SOFTWARE: PatentIn version 3.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 2385
19 <212> TYPE: DNA
20 <213> ORGANISM: HOMO SAPIEN
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (145)..(1032)
25 <223> OTHER INFORMATION:
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32 acccccagcc gggtgctccg agcc atg gcc gac acc atc ttc ggc agc ggg        171
33                            Met Ala Asp Thr Ile Phe Gly Ser Gly
34                            1               5
36 aat gat cag tgg gtt tgc ccc aat gac cgg cag ctt gcc ctt cga gcc       219
37 Asn Asp Gln Trp Val Cys Pro Asn Asp Arg Gln Leu Ala Leu Arg Ala
38 10                  15                  20                  25
40 aag ctg cag acg ggc tgg tcc gtg cac acc tac cag acg gag aag cag       267
41 Lys Leu Gln Thr Gly Trp Ser Val His Thr Tyr Gln Thr Glu Lys Gln
42                 30                  35                  40
44 agg agg aag cag cac ctc agc ccg gcg gag gtg gag gcc atc ctg cag       315
45 Arg Arg Lys Gln His Leu Ser Pro Ala Glu Val Glu Ala Ile Leu Gln
46             45                  50                  55
48 gtc atc cag agg gca gag cgg ctc gac gtc ctg gag cag cag aga atc       363
49 Val Ile Gln Arg Ala Glu Arg Leu Asp Val Leu Glu Gln Gln Arg Ile
50         60                  65                  70
52 ggg cgg ctg gtg gag cgg ctg gag acc atg agg cgg aat gtg atg ggg       411
53 Gly Arg Leu Val Glu Arg Leu Glu Thr Met Arg Arg Asn Val Met Gly
54     75                  80                  85
56 aac ggc ctg tcc cag tgt ctg ctc tgc ggg gag gtg ctg ggc ttc ctg       459
57 Asn Gly Leu Ser Gln Cys Leu Leu Cys Gly Glu Val Leu Gly Phe Leu
58 90                  95                  100                 105
60 ggc agc tcg tcg gtg ttc tgc aaa gac tgc agg aag gtc tgg aag agg       507
61 Gly Ser Ser Ser Val Phe Cys Lys Asp Cys Arg Lys Val Trp Lys Arg
62                 110                 115                 120
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68 aag acc cct ggc cga gct gat gag ccc cag ttc cga cct tgg ccc acg      603
69 Lys Thr Pro Gly Arg Ala Asp Glu Pro Gln Phe Arg Pro Trp Pro Thr
70         140                 145                 150
72 gaa ccg gca gag cga gag ccc aga agc tct gag acc agc cgc atc tac      651
73 Glu Pro Ala Glu Arg Glu Pro Arg Ser Ser Glu Thr Ser Arg Ile Tyr
74     155                 160                 165
76 acg tgg gcc cga gga aga gtg gtt tcc agt gac agt gac agt gac tcg      699
77 Thr Trp Ala Arg Gly Arg Val Val Ser Ser Asp Ser Asp Ser Asp Ser
78 170                 175                 180                 185
80 gat ctt agc tcc tcc agc cta gag gac aga ctc cca tcc act ggg gtc      747
81 Asp Leu Ser Ser Ser Ser Leu Glu Asp Arg Leu Pro Ser Thr Gly Val
82                 190                 195                 200
84 agg gac cgg aaa ggc gac aaa ccc tgg aag gag tca ggt ggc agc gtg      795
85 Arg Asp Arg Lys Gly Asp Lys Pro Trp Lys Glu Ser Gly Gly Ser Val
86             205                 210                 215
88 gag gcc ccc agg atg ggg ttc acc caa ccc gcg ggc cac ctc ttt ggg      843
89 Glu Ala Pro Arg Met Gly Phe Thr Gln Pro Ala Gly His Leu Phe Gly
90         220                 225                 230
92 ttg cag agc agc ctg gcc agt ggt gag acg ggc aca ggc tct gct gac      891
93 Leu Gln Ser Ser Leu Ala Ser Gly Glu Thr Gly Thr Gly Ser Ala Asp
94     235                 240                 245
96 ccg cca ggg gga ggg aca ggc tct gct gac ccg cca ggg gga ccc cgc      939
97 Pro Pro Gly Gly Gly Thr Gly Ser Ala Asp Pro Pro Gly Gly Pro Arg
98 250                 255                 260                 265
100 ccc ggg ctg acc cga agg gcc ccg gta aaa gac aca cct gga cga gcc      987
101 Pro Gly Leu Thr Arg Arg Ala Pro Val Lys Asp Thr Pro Gly Arg Ala
102                 270                 275                 280
104 ccc gct gct gac gca gct cca gca ggc ccc tcc agc tgc ctg ggc         1032
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106             285                 290                 295
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120 ctccgttgct atattaatgg caagactaaa tgaaacctag ggcacggcct ccgaagctgc   1452
122 gtgtggcccc ttagaggtga gcatcagagc cagagcagtg agggggagac tcacccaccc   1512
124 tctccctctc ccttcagctc tgggaggcag gcgcagtgcc cccctcccat gggctggccc   1572
126 aggaccgcgg gtgaaacctg ggtctgttta gtttctttgg tttttgtatg tttgtttgtt   1632
128 tttgacacag tctcgctttg ttgcccaggc tggggtgcag tggcacgatc gcggctcact   1692
130 gcaacctcca cctcccgggc tcaagcgatt ctctcacctc agcctcctga gtaggtggga   1752
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134 tccatgttgg ccaggctggt cttgaactcc tggtctcaag tgatccgccc gcctcggcct   1872
136 cccaaagtgc tgggattaca ggtgtgagcc accgcaccca atcctattag gtttctttga   1932
138 atcccctcat ggcctgcctg gtttttgctc agcctgtctt cagcttgagg agctgggaag   1992
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144 aaatacttca ttcagagtat gggcaaatgc ttctggaaaa cccttccctg aagagagaga   2172
146 acgtgtgtgt gtgtgtcggt gatcacaccc tcccatcctt cctgcctcct gccccaaacc   2232
148 ccgggttcct gggtctggaa gggccttctc tccaagctgg gagctcctgg gcccccacca   2292
150 ttcacttttt gtccttgctg ctggcaaaca gtaaagaaac tcactttccc tgtggcacgt   2352
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156 <211> LENGTH: 296
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167             20                  25                  30
170 Val His Thr Tyr Gln Thr Glu Lys Gln Arg Arg Lys Gln His Leu Ser
171         35                  40                  45
174 Pro Ala Glu Val Glu Ala Ile Leu Gln Val Ile Gln Arg Ala Glu Arg
175     50                  55                  60
178 Leu Asp Val Leu Glu Gln Gln Arg Ile Gly Arg Leu Val Glu Arg Leu
179 65                  70                  75                  80
182 Glu Thr Met Arg Arg Asn Val Met Gly Asn Gly Leu Ser Gln Cys Leu
183                 85                  90                  95
186 Leu Cys Gly Glu Val Leu Gly Phe Leu Gly Ser Ser Ser Val Phe Cys
187             100                 105                 110
190 Lys Asp Cys Arg Lys Val Trp Lys Arg Ser Gly Ala Trp Phe Tyr Lys
191         115                 120                 125
194 Gly Leu Pro Lys Tyr Ile Leu Pro Leu Lys Thr Pro Gly Arg Ala Asp
195     130                 135                 140
198 Glu Pro Gln Phe Arg Pro Trp Pro Thr Glu Pro Ala Glu Arg Glu Pro
199 145                 150                 155                 160
202 Arg Ser Ser Glu Thr Ser Arg Ile Tyr Thr Trp Ala Arg Gly Arg Val
203                 165                 170                 175
206 Val Ser Ser Asp Ser Asp Ser Asp Ser Asp Leu Ser Ser Ser Ser Leu
207             180                 185                 190
210 Glu Asp Arg Leu Pro Ser Thr Gly Val Arg Asp Arg Lys Gly Asp Lys
211         195                 200                 205
214 Pro Trp Lys Glu Ser Gly Gly Ser Val Glu Ala Pro Arg Met Gly Phe
215     210                 215                 220
218 Thr Gln Pro Ala Gly His Leu Phe Gly Leu Gln Ser Ser Leu Ala Ser
219 225                 230                 235                 240
222 Gly Glu Thr Gly Thr Gly Ser Ala Asp Pro Pro Gly Gly Gly Thr Gly
223                 245                 250                 255
226 Ser Ala Asp Pro Pro Gly Gly Pro Arg Pro Gly Leu Thr Arg Arg Ala
227             260                 265                 270
230 Pro Val Lys Asp Thr Pro Gly Arg Ala Pro Ala Ala Asp Ala Ala Pro
231         275                 280                 285
234 Ala Gly Pro Ser Ser Cys Leu Gly
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RAW SEQUENCE LISTING DATE: 08/07/2002
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245 <222> LOCATION: (145)..(1119)
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253 acccccagcc gggtgctccg agcc atg gcc gac acc atc ttc ggc agc ggg         171
254                            Met Ala Asp Thr Ile Phe Gly Ser Gly
255                            1               5
257 aat gat cag tgg gtt tgc ccc aat gac cgg cag ctt gcc ctt cga gcc         219
258 Asn Asp Gln Trp Val Cys Pro Asn Asp Arg Gln Leu Ala Leu Arg Ala
259 10                  15                  20                  25
261 aag ctg cag acg ggc tgg tcc gtg cac acc tac cag acg gag aag cag         267
262 Lys Leu Gln Thr Gly Trp Ser Val His Thr Tyr Gln Thr Glu Lys Gln
263                 30                  35                  40
265 agg agg aag cag cac ctc agc ccg gcg gag gtg gag gcc atc ctg cag         315
266 Arg Arg Lys Gln His Leu Ser Pro Ala Glu Val Glu Ala Ile Leu Gln
267             45                  50                  55
269 gtc atc cag agg gca gag cgg ctc gac gtc ctg gag cag cag aga atc         363
270 Val Ile Gln Arg Ala Glu Arg Leu Asp Val Leu Glu Gln Gln Arg Ile
271         60                  65                  70
273 ggg cgg ctg gtg gag cgg ctg gag acc atg agg cgg aat gtg atg ggg         411
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275     75                  80                  85
277 aac ggc ctg tcc cag tgt ctg ctc tgc ggg gag gtg ctg ggc ttc ctg         459
278 Asn Gly Leu Ser Gln Cys Leu Leu Cys Gly Glu Val Leu Gly Phe Leu
279 90                  95                  100                 105
281 ggc agc tcg tcg gtg ttc tgc aaa gac tgc agg aag aaa gtc tgc acc         507
282 Gly Ser Ser Ser Val Phe Cys Lys Asp Cys Arg Lys Lys Val Cys Thr
283                 110                 115                 120
285 aaa tgt ggg atc gag gcc tcc cct ggc cag aag cgg ccc ctg tgg ctg         555
286 Lys Cys Gly Ile Glu Ala Ser Pro Gly Gln Lys Arg Pro Leu Trp Leu
287             125                 130                 135
289 tgt aag atc tgc agt gag caa aga gag gtc tgg aag agg tcg ggg gcc         603
290 Cys Lys Ile Cys Ser Glu Gln Arg Glu Val Trp Lys Arg Ser Gly Ala
291         140                 145                 150
293 tgg ttc tac aaa ggg ctc ccc aag tat atc ttg ccc ctg aag acc cct         651
294 Trp Phe Tyr Lys Gly Leu Pro Lys Tyr Ile Leu Pro Leu Lys Thr Pro
295     155                 160                 165
297 ggc cga gct gat gac ccc cac ttc cga cct ttg ccc acg gaa ccg gca         699
298 Gly Arg Ala Asp Asp Pro His Phe Arg Pro Leu Pro Thr Glu Pro Ala
299 170                 175                 180                 185
301 gag cga gag ccc aga agc tct gag acc agc cgc atc tac acg tgg gcc         747
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306 Arg Gly Arg Val Val Ser Ser Asp Ser Asp Ser Asp Ser Asp Leu Ser
307             205                 210                 215
309 tcc tcc agc cta gag gac aga ctc cca tcc act ggg gtc agg gac cgg      843
310 Ser Ser Ser Leu Glu Asp Arg Leu Pro Ser Thr Gly Val Arg Asp Arg
311         220                 225                 230
313 aaa ggc gac aaa ccc tgg aag gag tca ggt ggc agc gtg gag gcc ccc      891
314 Lys Gly Asp Lys Pro Trp Lys Glu Ser Gly Gly Ser Val Glu Ala Pro
315     235                 240                 245
317 agg atg ggg ttc acc caa ccc gcg ggc cac ctc ttt ggg ttg cag agc      939
318 Arg Met Gly Phe Thr Gln Pro Ala Gly His Leu Phe Gly Leu Gln Ser
319 250                 255                 260                 265
321 agc ctg gcc agt ggt gag acg ggc aca ggc tct gct gac ccg cca ggg      987
322 Ser Leu Ala Ser Gly Glu Thr Gly Thr Gly Ser Ala Asp Pro Pro Gly
323                 270                 275                 280
325 gga ggg aca ggc tct gct gac ccg cca ggg gga ccc cgc ccc ggg ctg     1035
326 Gly Gly Thr Gly Ser Ala Asp Pro Pro Gly Gly Pro Arg Pro Gly Leu
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330 Thr Arg Arg Ala Pro Val Lys Asp Thr Pro Gly Arg Ala Pro Ala Ala
331         300                 305                 310
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334 Asp Ala Ala Pro Ala Gly Pro Ser Ser Cys Leu Gly
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339 gaccggtcct tgtgccctca ccagacaccc tgttggccat gactcaacaa accagtgttg   1249
341 ggagccgtct gcctccccag ctcagtgcct ttctgcaccc cttctctcct ggggagctgt   1309
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345 cctcccacac ccccaatcta cctggtgatg attttaagtt tgcgcgtgtc ttgggttggg   1429
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